

SEQUENCE LISTING

<110> Kufer Dr, Peter

<120> A novel method of identifying binding site domains that
retain the capacity of binding to an epitope

<130> B 3077 PCT

<150> EP 97 12 0096.9

<151> 1997-11-17

<160> 75

<170> PatentIn Ver. 2.0

<210> 1

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33

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aggtgtacac tccgatatcm arctgcagsa gtcwgg

36

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<212> DNA

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37

[illegible]

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<211> 96

<212> DNA

<213> Artificial Sequence

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ggcggcgccg gctccggtgg tgggtggttct caggtsmarc tgcagsagtc wggacctgag 60
ctggtgaagc ctggggcttc agtgaagatt tcttgc 96

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atttcctgc

69

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<211> 64

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ccag

64

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006767 5915560

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<211> 29

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aatccggatt tgatctcgag cttggtccc 29

<210> 12

<211> 22

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$\langle 220 \rangle$

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<210> 13

<211> 17

[illegible]

<212> DNA

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<400> 13

ctgaggagac ggtgacc

17

<210> 14

<211> 38

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24

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[illegible]

<211> 55

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Sequence: 1-79

9/48

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<400> 23

gcctccggaa gcattgacag gaggttgagg 30

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006101: 994550

10/48

<213> Artificial Sequence

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<400> 26

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<213> Artificial Sequence

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27

<210> 38

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<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

<400> 38

gaagtgaagc tcgaggagtc tggggga

27

<210> 39

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide

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gaggttcagc tcgagcagtc tggagct

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<210> 40

<211> 34

<212> DNA

<213> Artificial Sequence

[illegible]

<220>

<223> synthetic oligonucleotide

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tgaggagacg gtgaccgtgg tcccttggcc ccag

34

<210> 41

<211> 32

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<210> 42

<211> 32

<212> DNA

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32

<210> 43

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<211> 32

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32

<210> 44

<211> 32

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32

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<220>

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32

<210> 47

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32

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<211> 67

<213> Artificial Sequence

<223> synthetic oligonucleotide

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cattgag 67

67

<211> 42

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<223> synthetic oligonucleotide

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42

<211> 42

[illegible]

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[illegible]

85 90 95

Ala Lys Asp Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr

110

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Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

15

23/48

30

45

60

80

95

105

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<223> synthetic oligonucleotide

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24/48

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agcgctattc catatggacg tcccgcgcga ggtcgtccat catcaccatc atcactgagc 180
ggccgctcta gagtcgacct c 201

<210> 58

<211> 525

<212> DNA

<213> M13-Phage and artificial sequence of the MCS

<220>

<223> DNA-sequence of the N2-domain and the MCS

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cctaatacctt ctcttgagga gtctcagcct cttaataactt tcatgtttca gaataatagg 180
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ggtggatccg aggtgcagct gctcgagccc ggtcaccgtc tccctcaggtg gtggtggttc 480
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<210> 59

<211> 137

<212> PRT

<213> Artificial Sequence

<220>

<223> protein sequence M13 protein III and N2-domain

Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr

1 5 10 15

Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro

20 25 30

Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe

35 40 45

Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val

50 55 60

Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr

65 70 75 80

Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn

85 90 95

Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro

100 105 110

Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro

115 120 125

Val Asn Ala Ser Gly Gly Gly Gly Ser

130 135

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<213> Mus sp.

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agtaagagca	ttagcaaata	tttagcctgg	tatcaagaga	aacctgggaa	aactaataag	540
cttcttatct	actctggatc	cactttgcaa	tctggaattc	catcaagggt	cagtggcagt	600
ggatctggta	cagatttcac	tctcaccatc	agtagcctgg	agcctgaaga	ttttgcaatg	660
tattactgtc	aacagcataa	tgaatatccg	tacacgttcg	gagggggggac	caagcttgag	720
atcaaa						726

<210> 61

<211> 242

<212> PRT

<213> Mus sp.

<400> 61

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly

1

5

10

15

27/48

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35 40 45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

[illegible]

28/48

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly

180

185

190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210

215

220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

225

230

235

240

Ile Lys

<210> 62

<211> 753

<212> DNA

<213> Mus sp.

<400> 62

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agaactggac agggccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180
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tccatggagc tccgcagcct gacatctgag gactctgcgg tctatttctg tgcaagacgg 300
ggatcctacg gtagtaacta cgactggtac ttcgatgtct ggggccaaagg gaccacgggtc 360
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29/48

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ctgcagaagc caggccagtc tccaaagctc ctgatctaca aagttttccaa ccgatttttct 600
gggggtcccag acaggttcag tggcagtgga tcagggacag atttcacact caagatcagc 660
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acgttcggag gggggaccaa gcttgagatc aaa 753
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<213> Mus sp.

<400> 63

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1 5 10 15

Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser

20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp

35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys

50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe



30/48

85

90

95

Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp

100

105

110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly

115

120

125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr

130

135

140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile

145

150

155

160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr

165

170

175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile

180

185

190

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly

195

200

205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala

210

215

220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

225

230

235

240

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

[illegible]

31/48

245

250

<210> 64

<211> 726

<212> DNA

<213> Mus sp.

<400> 64

gaggtgcagc tgctcgagca gtctggagct gcgctggtaa ggcctgggac ttcagtgaag 60
atatactgca aggccttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatatttacc ctggaagtgg taatactcac 180
tacaatgaga gggttcagggg caaagccaca ctgactgcag acaaatactc gagcacagcc 240
tttatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacgggcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct ccagatgacc 420
cagtctccat cttatcttgc tgcattctct ggagaaacca ttactattaa ttgcagggca 480
agtaagagca ttagcaaata ttagcctgg tatcaagaga aacctgggaa aactaataag 540
cttcttatct actctggatc cactttgcaa tctggaattc catcaagggt cagtggcagt 600
ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcaatg 660
tattactgtc aacagcataa tgaatacccg tacacgttcg gaggggggac caagcttgag 720
atcaaa 726

<210> 65

<211> 242

<212> PRT

<213> Mus sp.

<400> 65

32/48

1 5 10 15

20 25 30

50 55 60

65 70 75 80

85 90 95

100 105 110

115 120 125

130 135 140

145 150 155 160

33/48

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly

165

170

175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly

180

185

190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu

195

200

205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln

210

215

220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu

225

230

235

240

Ile Lys

<210> 66

<211> 744

<212> DNA

<213> Mus sp.

<400> 66

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atatcctgca aggtttctgg atacgccttc actaactact ggctaggttg ggttaagcag 120
aggcctggac atggacttga atgggttgga gatattttcc ctggaagtgg taatgctcac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtcctc gtacacagcc 240
tatatgcagc tcagtagcct gacatctgag gactctgctg tctatttctg tgcaagattg 300

006707 33/48/33

65 70 75 80

85

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105

110

115

120

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130

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140

145

150

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160

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Gly Gly Thr Lys Leu Glu Ile Lys

245

<210> 68

<211> 726

<212> DNA

<213> Mus sp.

<400> 69

gaggtgcagc tgctcgagca gtctggagct gagctgggtga ggcctggggc ttcagtgaag 60
atatacctgca aggccttctgg atacgccttc aataactact ggctagggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gacatttacc ctggaagtgg aaatactcac 180
tacaatgaga gggttcagggg caaagccaca ctgactgcag acaaatacctc gagcacagcc 240
tttatgcagt taagtagcct gacatctgag gactctgctg tctatctctg tgcaagattg 300
aggaactggg acgaggctat ggactactgg ggccaaggga ccaaggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtcatgacc 420
cagtctccat cttatcttgc tgcattctct ggagaaacca ttactattaa ttgcagggca 480
agtaagagca ttagcaaata tttagcctgg tatcaagaga aacctgggaa aactaataag 540
cttcttatct actctggatc cactttgcaa tctggaattc catcaagggt cagtggcagt 600
ggatctggta cagatttcac tctcaccatc agtagcctgg agcctgaaga ttttgcaatg 660
tattactgtc aacagcataa tgaatacccg tacacgttcg gaggggggac caagcttgag 720
atcaaa 726

<210> 69

<211> 242

<212> PRT

<213> Mus sp.

37/48

<400> 69

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

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Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn

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Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

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Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg

50

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60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

65

70

75

80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe

85

90

95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100

105

110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

115

120

125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser

130

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Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala

145

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155

160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
225 230 235 240

Ile Lys

<210> 70

<211> 753

<212> DNA

<213> Mus sp.

<400> 70

gaggtgcagc tgctcgagca gtctggagct gagctggcga ggcctggggc ttcagtgaag 60
ctgtcctgca aggccttctg ctacaccttc acaaactatg gtttaagctg ggtgaagcag 120
aggcctggac aggtccttga gtggattgga gaggtttatc ctagaattgg taatgcttac 180

[illegible]

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala

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[illegible]

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215

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41/48

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr

225

230

235

240

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

245

250

<210> 72

<211> 717

<212> DNA

<213> Mus sp.

<400> 72

gaggtgcagc tgctcgagtc tggaggtggc ctggtgcagc ctggaggatc cctgaaactc 60
tcctgtgcag cctcaggatt cgattttagt agatactgga tgagttgggt ccggcagggt 120
ccagggaaag ggctagaatg gattggagaa attaatccag atagcagtac gataaactat 180
acgccatctc tgaaggataa attcatcatc tccagagaca acgccaaaaa tacgctgtac 240
ctgcaaatgg gcaaagtgag atctgaggac acagcccttt attactgtgc aagaggagcc 300
ttcctttttg actactgggg ccaagggacc acggtcaccg tctcctcagg tgggtggtggt 360
tctggcggcg gcggtcccg tgggtggtggt tctgagctcg tgctcaccca gtctccaacc 420
accatggctg catctcccgg ggagaagatc actatcacct gcagtgccag ctcaagtata 480
agttccaatt acttgcatcg gtatcagcag aagccaggat tctcccctaa actcttgatt 540
tataggacat ccaatctggc ttctggagtc ccagctcgct tcagtggcag tgggtctggg 600
acctcttact ctctcacaat tggcaccatg gaggtgaag atgttgccac ttactactgc 660
cagcagggta gtagtatacc actcacgttc ggtgctggga ccaagcttga gatcaaa 717

<210> 73

<211> 239

<212> PRT

<213> Mus sp.

42/48

<400> 73

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
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Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asp	Phe	Ser	Arg	Tyr	
			20					25					30			
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
		35				40						45				
Gly	Glu	Ile	Asn	Pro	Asp	Ser	Ser	Thr	Ile	Asn	Tyr	Thr	Pro	Ser	Leu	
	50					55					60					
Lys	Asp	Lys	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	
65				70						75				80		
Leu	Gln	Met	Gly	Lys	Val	Arg	Ser	Glu	Asp	Thr	Ala	Leu	Tyr	Tyr	Cys	
			85					90				95				
Ala	Arg	Gly	Ala	Phe	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	
		100						105				110				
Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
		115				120						125				
Gly	Gly	Ser	Glu	Leu	Val	Leu	Thr	Gln	Ser	Pro	Thr	Thr	Met	Ala	Ala	
	130					135					140					
Ser	Pro	Gly	Glu	Lys	Ile	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile	
145				150					155						160	
Ser	Ser	Asn	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Phe	Ser	Pro	
		165						170				175				
Lys	Leu	Leu	Ile	Tyr	Arg	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	
		180						185				190				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Gly	
	195					200						205				
Thr	Met	Glu	Ala	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Ser	

[illegible]

43/48

210 215 220
Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 74

<211> 744

<212> DNA

<213> Mus sp.

<400> 74

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggctgggac ttcagtgaag 60
atatactgca aggccttctgg atacgccttc actaactact ggctaggttg ggtaaagcag 120
aggcctggac atggacttga gtggattgga gatattttcc ctggaagtgg taatatccac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaaattcttc gagcacagcc 240
tatatgcagc tcagtagcct gacatttgag gactctgctg tctatttctg tgcaagactg 300
aggaactggg acgagcctat ggactactgg ggccaaggga ccacggtcac cgtctcctca 360
ggtggtggtg gttctggcgg cggcggctcc ggtggtggtg gttctgagct cgtgatgaca 420
cagtctccat cctccctgac tgtgacagca ggagagaagg tcactatgag ctgcaagtcc 480
agtcagagtc tgtaaacag tggaaatcaa aagaactact tgacctggta ccagcagaaa 540
ccagggcagc ctctaaact gttgatctac tgggcatcca ctagggaatc tggggtccct 600
gatcgcttca caggcagtgg atctggaaca gatttcactc tcaccatcag cagtgtgcag 660
gctgaagacc tggcagttta ttactgtcag aatgattata gttatccgct cacgttcggt 720
gctgggacca agcttgagat caaaa 744

<210> 75

<211> 248

<212> PRT

<213> Mus sp.

<400> 75

44/48

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

[illegible]

45/48

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys
245

<210> 76

<211> 744

<212> DNA

<213> Mus sp.

<400> 76

gaggtgcagc tgctcgagca gtctggagct gagctggtaa ggcctgggac ttcagtgaag 60
atatcctgca aggtctctgg atacgccttc actaactact ggctaggttg ggttaagcag 120
aggcctggac atggacttga atgggttggga gatattttcc ctggaagtgg taatgctcac 180
tacaatgaga agttcaaggg caaagccaca ctgactgcag acaagtcctc gtacacagcc 240

[illegible]

<213> Mus sp.

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly

1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn

20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp

35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys

50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala

65 70 75 80

1

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105

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120

125

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

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Gly Gly Thr Lys Leu Glu Ile Lys

245

TABLE 1		TABLE 2		TABLE 3		TABLE 4		TABLE 5		TABLE 6		TABLE 7		TABLE 8		TABLE 9		TABLE 10	
Data		Data		Data		Data		Data		Data		Data		Data		Data		Data	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100